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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=6t2-CM4-HT0652-150
400-143-h09&3=2000-04-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 134.

FEATURES

Location/Qualifiers
1..134

/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="HT0652"

/note="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 75; DB 10; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.7e-30;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCCACGAGGTTTCAGCTGCTCTTACTTTTAAACGAGTGAATGACCTGCCGCG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
7 ATGGCTCCACGAGGTTTCAGCTGCTCTTACTTTTAAACGAGTGAATGACCTGCCGCG 66

QY 61 AAGAGCGCGGCATGA 75
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
67 AAGAGCGCGGCATGA 81

RESULT 3

BM755441
LOCUS K-EST0033206 S11SN1 Homo sapiens cDNA clone S11SN1-13-B07 5',
DEFINITION 150 bp mRNA linear EST 04-MAR-2002

ACCESION BM755441

VERSION BM755441.1 GI:19085059

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 150)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.N., Park,H.S., Kim,S. and
Kim,Y.S.

21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS

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Email: yongsung@mail.kribb.re.kr

Plate: 13 row: B column: 07

High quality sequence stop: 150.

Location/Qualifiers

1..150

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S11SN1-13-B07"

/sex="M"

FEATURES

Location/Qualifiers
1..151

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S11SN1-13-B07"

/sex="M"

/dev_stage="45 years old"

/tissue type="Stomach"

/cell_type="Lymphoblast-like"

/cell_line="SNU-1"

/lab_host="Top10F"

/clone_lib="S11SN1"

/note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI;

Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then decapped

with tobacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including SfiI

site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized with Superscript II using SfiI

oligo-dT primer. After first strand synthesis, RNA was

degraded by NaOH treatment and cDNA was amplified by PCR

reaction. The PCR products were digested with SfiI and

cloned into DraIII- digested pME18S-FL3 vector. The

obtained cDNA vectors were used for transposition of

competent cells E. coli Top10F by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 75; DB 12; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCCACGAGGTTTCAGCTGCTCTTACTTTTAAACGAGTGAATGACCTGCCGCG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
5 ATGGCTCCACGAGGTTTCAGCTGCTCTTACTTTTAAACGAGTGAATGACCTGCCGCG 64

QY 61 AAGAGCGCGGCATGA 75
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
65 AAGAGCGCGGCATGA 79

RESULT 4

AA579497/c

LOCUS AA579497

DEFINITION H534603.S1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:915964, mRNA

sequence.

ACCESION AA579497

VERSION AA579497.1 GI:2357681

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 151)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquai,

M.D., Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 581 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 145.

Location/Qualifiers

1..151

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:915964"

/sex="Male"

/dev_stage="45 years old"

FEATURES

Location/Qualifiers
1..151

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:915964"

/sex="Male"

/dev_stage="45 years old"

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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr2"
/note="Vector: PAMPI0; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
ORIGIN
Query Match      100.0%; Score 75; DB 9; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCTCCACGAGGGTTCAGCTGCTCTTACTTTTAAACGAGTGAATTCACCTGCCCGTG 60
Db 96 ATGGCTCCACGAGGGTTCAGCTGCTCTTACTTTTAAACGAGTGAATTCACCTGCCCGTG 37
QY 61 AAGAGGGGGGCATGA 75
Db 36 AAGAGGGGGGCATGA 22

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RESULT 5
BE094504/c
LOCUS
DEFINITION
Accession
Version
Keywords
Source
Organism
Reference
Authors
Title
Journal
Medline
Pubmed
Comment

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Brazil
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMI-BT0769-080
500-216-g05&t3=2000-05-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 151.
Location/Qualifiers
1..151
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0769"

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/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from QRESTER PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
ORIGIN
Query Match      100.0%; Score 75; DB 10; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCTCCACGAGGGTTCAGCTGCTCTTACTTTTAAACGAGTGAATTCACCTGCCCGTG 60
Db 130 ATGGCTCCACGAGGGTTCAGCTGCTCTTACTTTTAAACGAGTGAATTCACCTGCCCGTG 71
QY 61 AAGAGGGGGGCATGA 75
Db 70 AAGAGGGGGGCATGA 56

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RESULT 6
BE164264/c
LOCUS
DEFINITION
Accession
Version
Keywords
Source
Organism
Reference
Authors
Title
Journal
Medline
Pubmed
Comment

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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-HT0464-220
300-093-e04&t3=2000-03-22&t4=1)
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High quality sequence stop: 156.
Location/Qualifiers
1..156
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0464"
/note="Organ: head neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from QRESTER PCR (U.S. Letters patent application
No.196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under

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